Amendments to the Specification:

On page 1, before line 1, insert:

--RELATED APPLICATION

This application is a continuation of United States Patent Application Serial No. 09/976,787, filed October 12, 2001, which is a continuation of United States Patent Application Serial No. 09/493,539, filed January 28, 2000, which claims the benefit of United States Provisional Patent Application Serial No. 60/117,726, filed January 29, 1999, herein incorporated by reference in its entirety.--

Please replace the paragraph at page 7, lines 15 to 24 with the following text:

The peptide linkers used to produce the single chain antibodies may be flexible peptides selected to assure that the proper three-dimensional folding of the V_L and V_H domains may occur once they are linked so as to maintain the target molecule binding-specificity of the full length anti-KDR antibody. Generally, the carboxyl terminus of the V_L or V_H sequence may be covalently linked by such a peptide linker to the amino acid terminus of a complementary V_H or V_L sequence. The linker is generally 10 to 50 amino acid residues. Preferably, the linker is 10 to 30 amino acid residues. More preferably the linker is 12 to 30 amino acid residues. Most preferably is a linker of 15 to 25 amino acid residues. An example of such linker peptides include $(Gly\text{-}Gly\text{-}Gly\text{-}Gly\text{-}Ser)^3$ (SEQ ID NO:17).

Please replace the paragraph at page 9, lines 1 to 9 with the following text:

Two single chain antibodies can be combined to form diabodies, also known as bivalent dimers. Diabodies have two chains. Each chain of the diabody includes a V_H domain connected to a V_L domain. The domains are connected with linkers that are short enough to prevent pairing between domains on the same chain, thus driving the pairing between complementary domains on different chains to recreate the two antigen-binding sites. The peptide linker includes at least five amino acid residues and no more than ten amino acid residues, e.g. (Gly-Gly-Gly-Gly-Ser), (SEQ ID NO:21), $(Gly\text{-}Gly\text{-}Gly\text{-}Gly\text{-}Ser)_2$,

(SEQ ID NO:19). The diabody structure is rigid and compact. The antigen-binding sites are at opposite ends of the molecule. Diabodies may be monospecific or bispecific.--

Please replace the paragraph beginning at page 13, line 26 and ending at page 14, line 4 with the following text:

In displaying the scFv on filamentous pge surface, antibody V_H and V_L domains are joined together by a 15 amino-acid-long linker $(GGGGS)^3$ (SEQ ID NO:17) and fused to the N-terminal of phage protein III. A 15 amino-acid-long E tag, which is followed by an amber codon (TAG), was inserted between the C-terminal of V_L and the protein III for detection and other analytic purposes. The amber codon positioned between the E tag and the protein III enables the construct to make scFv in surface-displaying format when transformed into a suppressor host (such as TG1 cells), and scFv in soluble form when transformed into a nonsuppressor host (such as HB2151 cells).

Please replace the text starting at page 19, line 12 up to and including page 19, line 22 with the following text:

Primer 1: 5' CTA GTA GCA ACT GCA ACT GGA GTA CAT TCA GAC ATC GAG CTC 3' (SEQ ID NO:36)
Primer 2: 5' TCG ATC TAG AAG GAT CCA CTC ACG TTT TAT TTC CAG 3'
*Bam*H I
(SEQ ID NO:37)
Primer 3: 5' CTA GTA GCA ACT GCA ACT GGA GTA CAT TCA CAG GTC AAG CTG 3' (SEQ ID NO:38)
Primer 4: 5' TCG AAG GAT CCA CTC ACC TGA GGA GAC GGT 3' (SEQ ID NO:39)
*Bam*H I
Primer 5: 5' GGT CAA AAG CTT ATG GGA TGG TCA TGT ATC ATC CTT TTT
Hind III
CTA GTA GCA ACT 3' (SEQ ID NO:40)